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Taxonomy

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File

 1: CAD58967. Disease resistanc...[gi:26986180]

BLink, Domains, Links

LOCUS CAD58967 318 aa linear **PLN** 15th DEC 2002
DEFINITION Disease resistance protein NBS-LRR type [Musa acuminata].
ACCESSION CAD58967
VERSION CAD58967.1 GI:26986180
DBSOURCE embl locus MAC534312, accession AJ534312.1
KEYWORDS
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE 1 (residues 1 to 318)
AUTHORS Arango, R., Rodriguez, E. and May, G.D.
TITLE Partial cloning of a disease resistance gene analog from Musa
acuminata (Var. Grand Nain)
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 318)
AUTHORS Arango, R.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-2002) Grupo de Biotecnologia Vegetal UNALMED-CIB,
Carrera 72 A No. 78B- 141, Medellin, Antioquia, COLOMBIA
FEATURES Location/Qualifiers
source 1..318
/organism="Musa acuminata"
/cultivar="Grand Nain"
/db_xref="taxon:4641"
Protein 1..318
/product="Disease resistance protein NBS-LRR type"
Region 137..>304
/region_name="NB-ARC domain"
/note="NB-ARC"
/db_xref="CDD:24492"
CDS 1..318
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/coded_by="AJ534312.1:<1..957"
/db_xref="GOA:Q8GUB6"
/db_xref="UniProt/TrEMBL:Q8GUB6"
ORIGIN
1 vhdeiketlt acfqrlrrtrn sltealsdlr ataqrvkdkv eeeeahqric npdvrrwqkk
61 vdeilrecda ggeheepkrc aclcgcdmdl lhrhrvarkv vqnlgdvnkl ksdgdaftpp
121 fnhepppepv eelpfetgti gmelalsql1 srfdeaeksi ighvglggvg ktllktlnn
181 elkentrdyh vvimievans etlnvvdmqk iianrlalpw neseterers tylrralrrk
241 kfvvlddvw kkfqladvgi ptppssdkgck lilasrsnqv cvemgdkepm empclgdnes
301 lrlfpeqldg rgqcrhrp
//



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000! wordsize: 3

Filter Align

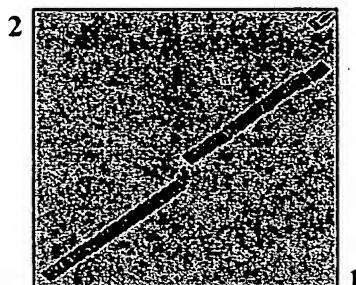
Prior art

claimed

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1 SEQ ID NO: 42 x SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEQLNDKPLENWLQKLNAATYEVDDILDEYKTKATRF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI
Sbjct: 52 SLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAIRLKVRSTFKRLIDHVII 111

Query: 99 --PFRHKVGKRMQVMKKLNAAEERK-NFHLQEKKIERQAATRE-TGSVLTEPQVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR
Sbjct: 112 NVPLAHKVA---DIRKRLNGVTLERELNLGALEGSQPLDSTKRGVTTSLTESCIVGRA 167

Query: 155 KEKDEIVKILINNSDAQKLSVLPILGMGGLGKTTLSQMVFNDQRVTERFYPKIKWICVSD 214
++K+ +++L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD
Sbjct: 168 QDKENLIRLLLEPSDGA--VPVPIVGLGGAGKTTLSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRLIKAIVE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDVWNEDQHKWANL 273
DFD KR+ + I E + G+ + +L LQ L+E + G + LVLDDVWNED KW +L
Sbjct: 226 DFDVKRITREITEYATNGRFMDLTNLNMLQVNLKEEIRGTTFLVLDDVWNEDPVWKWESL 285

Query: 274 RAVLKVGASGAFVLTTRLEKVGSIIMGTLQPYELSNLSPEDCWFLFMQRAFGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N
Sbjct: 286 LAPLDAGGRGSVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIESHSFREASCSSTN 345

Query: 332 PNLVAIGKEIVKKCGGVPLAAKTLGGILRKFREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR
Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAADVLSALR 405

Query: 391 LSYHHLPLDLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+
Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPSLLQK----- 463
N V N+ Y R SP + K
Sbjct: 466 VCRFFFYRYSWGNVMNDSVHDLARWVSLDEYFRADEDSPFHISKPIRHLWCERITNVL 525

Query: 464 -----FXXXXXXXXXXXXQLPSSI 484
LPSS+

Subject: 526 EDNNNTGGDAVNPLSSLRLLFLGQSEFRSYHLLDRMFRMLSRIRVLDNSNCVIRNLPSSV 585

Query: 485 GDLVHLYLDLSGNFRIRNLPKRLCKLQNLQTLSDLHYCDSLSCLPKQTSKLGSLRNLLD 544
G+L HLYYL LS N RI+ LP+ + L LQTL L C+ L LP+ S+L LR L +

Subject: 586 GNLKHLRYLGLS-NTRIQLPESVTRLCLLQTLLEGCE-LCRLPRSMSRLVQLRQLKAN 643

Query: 545 GCSLTSTPPRIGLLTCLKSLSFCVIGKRKGYQLGELKNLN-LYGSISITKLDdrvKKDSDA 603
+ + + + G L L+ L + + K+KG+ + EL +N L+G +SI L V+K ++

Subject: 644 P-DVIADIAKVGRILIELQELKAYNVDDKKKGHIAELSAMNQLHGDLSIRNLQNEKTRES 702

Query: 604 KEANLSAKANLHSCLSWLDGKHR---YDSEVLEALKPHSNLKYLEINGFGGIRLPDW 659
++A L K L L L W DG+ D +VL+ L+PH NL+ L I +GG P W

Subject: 703 RKARLDEKQKLKLLDLRW-ADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSW 761

Query: 660 MNQSVLKNNVSIRIRGCENCSCLPFGELPCLESLELHTGSADVEYVEDNVH---PGRF 715
M L N+ +IR+R C + LP G+L L L + G + V + + F

Subject: 762 MTDQYLPNMETIRLRSCARLTELPCCLGQLHILRHLHI-DGMSQVRQINLQFYGTGEVSGF 820

Query: 716 PSLRKLVIWDFSNLKGLLK-KEGEEQFPVLEEMTFYWCP-MFVIPTLSSVKTLKVIATDA 773
P L L I +L+ + + FP L ++ CP + +P+L TL+ +

Subject: 821 PLLELLNIRRMPGLEEWSEPRRNCCYFPRLHKLIEDCPRLRNLPSP--PTLEELRISR 878

Query: 774 TVLRSISNLRALTSLDISNNVEATSLPEEMFKSLANLKYLNISFFRNLKELPTXXXXXX 833
T L + + D++ NV +SL + L +L + NL L T

Subject: 879 TGLVDLPGFHG--NGDVTTNVSLSSLHVSECRELRLSEGLLQ--HNLVALKT----- 927

Query: 834 XXXXXFEFCNALESPLPAEGVKGLTSLTELSVSNCMMLKC---LPEGLQH 879
F C++LE LPAEG + SL L ++NC L C LP L+H

Subject: 928 ---AAFTDCDSLEFLPAEGFRTAISLESLIMITNC-PLPCSFLLPSSLEH 972

Score = 43.9 bits (102), Expect = 0.036

Identities = 24/75 (32%), Positives = 37/75 (49%), Gaps = 1/75 (1%)

Query: 842 CNALESPLPAEGVKGLTSLTELSVSNCMMLKCLPEGLQHXXXXXXXXQCPIVKRCERGI 901
C LE LPA ++ L SL+ L + C + P G +CP + +RC+
Subject: 1148 CPNLEVLPAN-LQSLCSLSTLYIVRCPRIHAFPPGGVMSLAHLVIHECPQLCQRCDPG 1206

Query: 902 GEDWHKIAHIPYLTL 916

G+DW IA++P + L

Subject: 1207 GDDWPLIANVPRICL 1221

CPU time: 0.16 user secs. 0.00 sys. secs. 0.16 total secs.

Lambda K H
0.320 0.137 0.410

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7820

Number of extensions: 5118

Number of successful extensions: 24

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 7

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918

Length of database: 765,028,816

Length adjustment: 140

Effective length of query: 778

Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

 Filter Align

Prior art

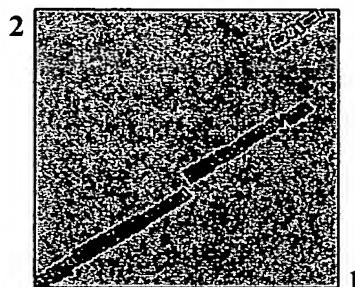
claimed

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1

SEQ ID NO: 42 x SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 375 bits (964), Expect = e-102

Identities = 286/950 (30%), Positives = 437/950 (45%), Gaps = 155/950 (16%)

Query: 2 AEAIFIQVVLNDNLTSFLKGELVLLFGFQDEFQ-LSSMFSTIQAVALEDAQEKLNDKPLEN 59
 A++FIQ +LD ++ +L G D+ + L + I A+L+ A+ + + L

Sbjct: 12 AQSFIQTLLDKASNCAIQQLARRRGLHDDLRLRLRTSLLRIHAILDKAETRWNHKNTSLVE 71

Query: 60 WLQKLNAAATYEVDDILDEYKTKATRFLQSEYGRYHPKVIPFR-----HKVGKR 107
 + + + L A Y+ + D+L+E + +A + G + F G R

Sbjct: 72 LVRQLKDAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTASEWLGADGDDAGTR 131

Query: 108 MDQVMKKLNAAIAEERKNFHQL-----EKIIERQAATRETGSVLTEPQVYGRDKEKDEIV 161
 + ++ KL IA + + + + + RET S LTE V+GRD+E+++V

Sbjct: 132 LREIQGKLCNIAADMMMDVMQLLAPDDGGRQFDWKVVRRETSSFLTETVVFGRDQEREKVV 191

Query: 162 KILINNVSDAQKLSVLPILGMGGLGKTTLSQMVNDQRVTERFYPKIKIWIICVSDDFDEKRL 221
 ++L+++ S SVLP++G+GG+GKTTL+Q+V+ND RV F+ K+W+CVSD+F+ KRL

Sbjct: 192 ELLLDGSGNSSFVPLVIGGGVGKTTLAQLVYNDNRVGNYFHLKVWVCVSDNFNVKRL 251

Query: 222 IKAIVESIEGKSLSD-MDLAPLQKKLQELLNGKRYFLVLDVWNEDQHKWANLRAVLKVG 280
 K I+ES SD ++L LQ+ L+E + +R+ LVLDDVW+E++ W L A L+

Sbjct: 252 TKEIIIESATKVEQSDKLNLDLQQILKEKIASERFLLVLDVWSENRRDDWERLCAPLRFA 311

Query: 281 ASGAFVLTTRLEKVGSIIMGTLPYELSNLSPEDCWFLFMQRAGHQEEINP---NLVA 336
 A G+ V+ TTR K+ SI+GT++ L L + W LF + AFG +NP L

Sbjct: 312 ARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAFG---SVNPQEHLLEV 368

Query: 337 IGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDESSILPALRLSYHH 395
 IG++I K G PLAAKTLG +LR + W + +S +W LPQ E+ ILP L LSY H

Sbjct: 369 IGRKIAGKLKGSPPLAAKTLGSLLRLDVSEHWRTIMESEVWQLPQAENEILPVLWLSYQH 428

Query: 396 LPLDLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----NEVWNELY 450
 LP L QCF +CAVF KD K LI W+A GF+ +GN +EDV +E+ N +

Sbjct: 429 LPGHLRQCFCAFVFKDYLFYKHELIQTWIAEGFIAHQGNKRMEDVGSSYFHELVNRSF 488

Query: 451 LRVSSY----- 456
 + S +

Sbjct: 489 FQESRWRGRYVMHDLIHDLAQFISVGECRIRDDKSKETPSTTRHLSVALTEQMKLVDFS 548

Query: 457 -----SPSLLQKFXXXXXXXXXXXXQLPSSIGDLV 488
SL ++ +LP IGDL+

Sbjct: 549 GYNKLRTLMINNQRNQYPYMTKVNSCLPHSLFKRLKRIHVVLQKCGMKELPDIIGDLI 608

Query: 489 HLRYLDLSGNFRIRNLPKRLCKLQNLQTLSDLHYCDSLSCLPKQTSKLGSLRNLLDGCSL 548
LRYLD+S N I+ LP+ LC L NLQ L L C L P+ SKL +LR L ++ +

Sbjct: 609 QLRYLDISYNACIQRLPESLCDLYNLQALRLWGC-QLRSFPQGMSKLINLRQLRVED-EI 666

Query: 549 TSTPPRIGLLTCLKSLSCFVIGKRKGYQLGELKNL-NLYGSISITKLDRVKKDSAKEAN 607
S +G L L+ LS F + G +L EL L L ++ IT L+ V +A +A

Sbjct: 667 ISKIYEVGKLISLQELSAFKVLNNHGNKLAELSGLTQLRSTLRITNLENVGSKEEASKAK 726

Query: 608 LSAKANLHSLCLS-----DLDGKHRYDSEVLEALKPHSNLKYLEINGFGGIRLPDWMN 661
L K L +L L W L+ + EVL L+PH LK L I G+ G +P W++

Sbjct: 727 LHRKQYLEALELEWAAGQVSSLEHELLVSEEVLLGLQPHHFLKSLTIRGYSGATVPSWLD 786

Query: 662 QSVLKNNVSIRIRGCENCSCLPFGELPCLESLELHTGSADVEYVEDNVH-----PGR 714
+L N+ +++ C L G+LP L+ L+ + V+ H

Sbjct: 787 VKMLPNLGLTLKLENCTRLEGLSYIGQLPHLKVLHMKR---MPVVKQMSHELCGCTKSKL 842

Query: 715 FPSLRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVIPTLSSVKTLKVIATDAT 774
FP L +LV+ D LK +FP L+ +P L+ + A

Sbjct: 843 FPRLEELVLEDMPTLK-----EFPNLAQ-----LPCLKIIMKKNMFAVKHI 883

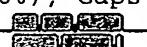
Query: 775 VLRSISNLRALTSDLISNNVEATSLPEEMFKSLANLKYLNISFFRNLKEL 824

++ + L+ V L E +L L+L+ +N+ L

Sbjct: 884 GRELYGDIESNCFLSLEELVLQDMLTLEELPNLQQLPHLKVIHMKNMSAL 933

Score = 38.9 bits (89), Expect = 1.2

Identities = 38/162 (23%), Positives = 66/162 (40%), Gaps = 16/162 (9%)



Query: 718 LRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVI---PTLSSVKTLKVIATDAT 774
L++L N GL EG + L+ + CP ++ V +L ++ D T

Sbjct: 1258 LKELGTVRIENCGLGSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKT 1317

Query: 775 VLRSISNLRALTSDLISNNVEATSLPE-----EMFKSLANLKYLNISFFRNLKELP 825
L +S ++ +L +++ P+ E+ SL L+ L +NL+ LP

Sbjct: 1318 ALLKLSLIK--NTLPFIHSLRIIWSPQKVMFDLEEQELVHSLTALRRLEFFRCKNLQSLP 1375

Query: 826 TXXXXXXXXXXXXFECNNALESLPAEGVKGLTSLTELSVSNC 867

T C ++SLP +G+ T LT+L +C

Sbjct: 1376 TELHTLPSLHALVVSDCPQIQSLPEKGLP--TLLTDLGFDHC 1415

CPU time: 0.22 user secs. 0.00 sys. secs 0.22 total secs.

Lambda K H
0.320 0.137 0.410

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9464

Number of extensions: 6271

Number of successful extensions: 20

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 10

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918
Length of database: 765,028,816
Length adjustment: 140
Effective length of query: 778
Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



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Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 | expect: 10.000 | wordsize: 3

Filter Align

PRIOR ART

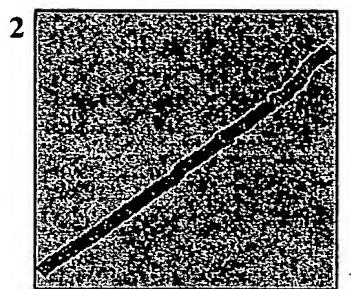
CLAIMED

Sequence 1 lcl|seq_1 Length 942 (1 .. 942)

D1 SEQ ID NO: 43

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 403 bits (1035), Expect = e-110

Identities = 309/998 (30%), Positives = 486/998 (47%), Gaps = 126/998 (12%)

Query: 23	DDILDDCKTEAARFK--QAVLGRYHPRITFCYKVGKRMKEMMEKLDIAEERR-NFHLD 79
Sbjct: 82	DDILD+ + A R K + + R I + + + + + + L+ + ER N
Query: 80	ERIIERQAARRQ-TGFVLTEPKVYGREKEEDEIVKILINNVSYSEEVPVLPILGMGGLGK 138
Sbjct: 141	E + + R T + LTE + GR + + + + + + L+ + VPV+PI+G+GG GK
Query: 139	EGSQPLDSTKRGVTTSLTESCIVGRAQDKENLIRLLLEPSDGA--VPVPIVGLGGAGK 198
Sbjct: 199	DDILDEYEAAAIRLKVTRSTFKRLIDHVI-INVPLAHKVADIRKRLNGVTLERELNLGAL 140
Query: 198	TTLAQMVFNDQRITEHFNLKIWVCVSDDFDEKRLIKAIIVE-SIEGKSLGDMDLAPLQKKL 197
Sbjct: 259	TTL+Q++FND+R+ EHF L++WVCVSDDFD KR+ + I E + G+ + +L LQ L
Query: 258	TTLSQLIFNDKRVEEHFPLRMWVCVSDDFDVKRITREITEYATNGRFMDLTNLNMLQVNL 258
Sbjct: 319	TTL+Q++FND+R+ EHF L++WVCVSDDFD KR+ + I E + G+ + +L LQ L
Query: 316	TTLSQLIFNDKRVEEHFPLRMWVCVSDDFDVKRITREITEYATNGRFMDLTNLNMLQVNL 258
Sbjct: 379	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Query: 376	QELLNGKRYFLVLDDVWNEDQEKWDNLRAVLKIGASGASILITTRLEKIGSIMGTLQLYQ 257
Sbjct: 439	+E + G + LVLDDVWNED KW++L A L G G+ + +TT+ +K+ + GT++ Y
Query: 431	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Sbjct: 494	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Query: 474	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Sbjct: 553	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Query: 532	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318
Sbjct: 592	KEEIRGTTFLLVLDDVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYV 318

Sbjct: 554 SYHLLDRMFRMLSRIRVLDFSNCVIRNLPSVGNLKHLRYLGLSNTRIQRLPESVTRLCL 613
 Query: 533 LQTLDLYNCQSLSLPKQTSKLCRLRNVLQDHCPLTSMPPIGLLTKLGYFVVGK 592
 Sbjct: 614 LQTLLLEGCE-LCRLPRSMSRLVQLRQLKANPDVIADI-AKVGRILIELQELKAYNVDKKK 671
 Query: 593 GYQLGELRNLN-LRGAISITHLERVKNDMEAKEYEANLSAKANLHSLSMSW-DRPNRYESE- 649
 Sbjct: 672 GHGIAEELSAMNQLHGDSLIRNLQNVETRESRKLARLDEKQKLKLLDLRWADGRGAGECDR 731
 Query: 650 EVKVLEALKPHPNLKYLEIIFCGFCLPDWMNHSVLKNVVSILISGCENCSCLPPFGELP 709
 Sbjct: 732 DRKVLLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSCARLTELPCLGQLH 791
 Query: 710 CLESLELQDGSVVEYV-----EDSGF-----LTRRRFPSSLRKLHIGGFCNLKGLQR 756
 Sbjct: 792 ILRHLHI-DGMSQVRQINLQFYGTGEVSGFPLLELLNIRRMPSELLEWS-----EP 840
 Query: 757 MKGAEQFPVLEEMKISDCPMF-----VFPTLSSVKKLE-----IWGEADAGGXXXX 803
 Sbjct: 841 RRNCCYFPRLHKLLIEDCPRLRNLPSPPTLEELRISRTGLVDPFGFHNGDVTNVSL 900
 Query: 804 XXXXXXXXKIFS-----NHTVTSLLLEEMFK-----NLENLI----- 834
 Sbjct: 901 SLHVSECRELRLSLEGLLQHNLVALKTAATDCDSLEFLPAEGFRTAISLESIMTNCP 960
 Query: 835 ---YLSVSFLENLK-----ELPTSLASLNNLKCLDIRYCYAXXXXXXXXXXXXX 879
 Sbjct: 961 PCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDIKDCPNLSSFPPGQLCQL 1020
 Query: 880 XXXXXXFVEHCNMLKCLPEGLQHLLTSLKIRGCPQL 917
 Sbjct: 1021 SALQHLSLVNCQRLQSI--GFQALTSLESLTIQNCPR 1056

CPU time: 0.09 user secs. 0.00 sys. secs 0.09 total secs.

Lambda K H
0.321 0.138 0.416

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 7971
 Number of extensions: 5184
 Number of successful extensions: 25
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's gapped: 2
 Number of HSP's successfully gapped: 1
 Number of extra gapped extensions for HSPs above 10.0: 0
 Length of query: 942
 Length of database: 765,028,816
 Length adjustment: 140
 Effective length of query: 802
 Effective length of database: 765,028,676
 Effective search space: 613552998152
 Effective search space used: 613552998152
 Neighboring words threshold: 9
 Window for multiple hits: 0
 X1: 16 (7.4 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.9 bits)

S2: 82. (36.2 bits)



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Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

Filter Align

PRIOR ART

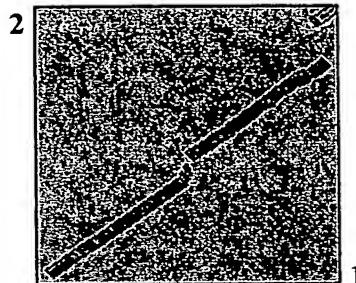
CLAIMED

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D/ SEQ ID NO: 2

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEQLNDKPLENLWQKLNAATYEVDDILDEYKTATRFF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI

Sbjct: 52 SLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKVTRSTFKRLIDHVI 111

Query: 99 --PFRHKVGKRMQVMKKLNAAEERK-NFHLQEKKIERQAATRE-TGSVLTEPQVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR

Sbjct: 112 NVPLAHKVA---DIRKRLNGVTLEREELNLAGLEGSQPLDSTKRGVTTSLTESCIVGRA 167

Query: 155 KEKDEIVKILINNVSDAQKLSVLPILGMGGLGKTTLSQMVFNDQRVTERFYPKIWICVSD 214
++K+ +--+L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD

Sbjct: 168 QDKENLIRLLLEPSDGA--VPVPIVGLGGAGKTTLSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRRIKAIYE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDVWNEDQHKWANL 273
DFD KR+ + I E + G+ + +L LQ L+E + G + LVLDDVWNED KW +L

Sbjct: 226 DFDVKRITREITEYATNGRFMDLTNLNMLQVNLKEEIRGTTFLVLDDVWNEDPVKWEGL 285

Query: 274 RAVLKVGASGAFVLTTRLEKVGSIMGTLQPYELSNLSPEDCWFLFMQRAFGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N

Sbjct: 286 LAPLDAGGRGSVVIVTTQSKVADVTGTMEPYVLEELTEDDSWSLIESHSFREASCSTN 345

Query: 332 PNLVAIGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR

Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAASDVLALAR 405

Query: 391 LSYHHLPLLDQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+

Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPSLLQK----- 463
N V N+ Y R SP + K

Sbjct: 466 VCRFFFYRYSWGNVVMNDSVHDLARWVSLDEYFRADEDSPHLHISKPIRHLWCERITNVL 525

Query: 464 -----FXXXXXXXXXXXXQLPSSI 484
LPSS+



Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits) **
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 | Mismatch: -2 | gap open: 5 | gap extension: 2
x dropoff: 50 expect: 10.000! wordsize: 11 Filter Align

Bior Art

Claimed

D2

SEQ ID NO: 1

Sequence 1 lcl|seq_1 Length 6658

Sequence 2 lcl|seq_2 Length 4380

No significant similarity was found



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 | Mismatch: -2 | gap open: 5 | gap extension: 2

x_dropoff: 50 | expect: 10.000 | wordsize: 11 | Filter |

*Prior Art**Claimed**D2**SEQUENCE:3*

Sequence 1 lcl|seq_1 Length 6658

Sequence 2 lcl|seq_2 Length 3660

No significant similarity was found



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 | expect: 10.000 | wordsize: 3 | Filter |

Claimed

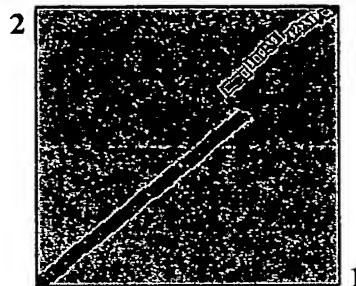
Prev Art

SEQ IDNO: 2

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

Query: 1 MEIGLAVGG AFLSSALNVLFDR LAPNGD LNMFRXXXXXXXXXXMTL RG IQIVL SDA 60
 M L +GG F S + L D+ A N + + R LR I +L A
 Sbjct: 1 MSTALVIGGWFAQSFIQTL LDK-ASNCAIQQLARRGLHDDLRLRTSLLR-IHAILDKA 58

Query: 61 ENK-QASNPSVRDWLNE LRD AVDSAENLIEEV NYEALRLKVEGQHQN FSETS NQQVS--- 116
 E + N S+ + + +L+DA AE+L+EE+ Y+A + KVE + S+ + +S
 Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQA AKQKVEH RGDQISDLFSFSLSTAS 118

Query: 117 -----DDFFLN IKDKLED TIETL KDLQEQI GLLGLKE---YFDSTKLETRRPSTS VDD 166
 DD + + + D+ + + LL + FD + RR ++S
 Sbjct: 119 EWLGADGDDAGTRLREI QGKLCNIAADMMDVMQLLAPDDG GRQFDW KV--RRETSSFLT 176

Query: 167 ESDIFGRQSEIE D LIDR LLSEGASGKKLTVVPIVGMGGQGKTTLA KAVYND E R VKNHFDL 226
 E+ +FGR E E + + + LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L
 Sbjct: 177 ETVVFG RDQEREK VVELL DSGSGN SFSV LPLVGIGGVGKTTLA QLVYNDNRVG NYFHL 236

Query: 227 KAWYC VSEGFD ALRIT KELLQ EIGKF DSKDV HNNLNQ LQVKL KESLKG KKF LIVL DDVWN 286
 K W CVS+ F+ R+TKE++ + K + D NL+ LQ LKE + ++FL+VL DDVW+
 Sbjct: 237 KVWVCVSDNFNVKRLTKEII E SATK VEQSD-KLNLD TLQ QILKE KIASER FLLV LDDVWS 295

Query: 287 ENYNEWNDLRNIFAQGDIGSKI I VTT RKS VALMMGN-EQIRMGNLSTEASW SLFQRHAF 345
 EN ++W L GSK+IVTTR +A ++G ++I + L +A W LF++ AF
 Sbjct: 296 ENRDDWERLCAPL RFAARGSKV I VTT RDTK I ASI I GTMKEISLDGLQDDAYWELFKKCAF 355

Query: 346 ENMDPMGH PEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEE WKRILRSEI WELP--H 403
 +++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP
 Sbjct: 356 GSVNPQEHLELEVIGRK IAGKLKG SPLA KTLG SLLR LDVS QEH WRTIME SEVW QLPQAE 415

Query: 404 NDILPALMLS YNDLPAHLKRCFS C A IFPKDYPFRKEQV IHLW IANGL VPK-DEIN QDL 462
 N+ILP L LSY LP HL++CF+FCA+F KDY F K ++I WIA G + + ++ +D+
 Sbjct: 416 NEILPVLWLSYQHLP GHLRQCF A FCAV FHKDYL FYKHELI QT WIAEGFIAHQGNKRMEDV 475

Query: 463 GNQYFLELRSRS LFEK VNP SKRNIEELFLMHD L VNDLA QLASS KLCIRLE E S QGSHM L E 522
 G+ YF EL +RS F+ + ++MHD L++DLAQ S C R+++ +

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 13,460
Number of extensions: 8847
Number of successful extensions: 46
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



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Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3

Filter

Align

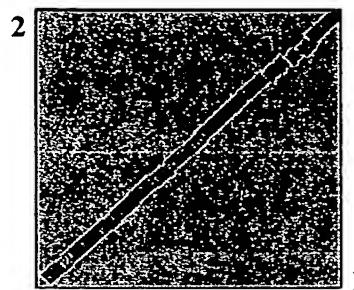
Prior Art

Claimed

D2

SEQ ID NO: 4

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)



Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49	TLRGIQIVLSDAENKQASNPSVRDWLNELRDAVDSAENLIEEVNYEALRLKVEGQHQNF	108
TL	+L +A+ ++ ++	WL EL++ A+++++E A+RLKV +
Sbjct: 46	TLLRTHSLLLEEAKARRMTDKSLLWLMELKEWAYDADDILDEYEAAAIRLK	V-----T 98
Query: 109	ETSNQQVSDDFFLNIK--DKLEDTIETLKDL---QEIQIGLLGLKEYFDSTKLETRRPST	162
++ ++ D	+N+ K+ D + L + + +G L + DSTK R +T	
Sbjct: 99	RSTFKRLIDHVIIINVPLAHKVADIRKRLNGVTLERELNLGALEGSQLDSTK	--RGVTT 155
Query: 163	SVDDESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKAVYNDERVK	222
S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+		
Sbjct: 156	SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVVPPIVGLGGAGKTTLSQLIFNDKR	VEE 213
Query: 223	HFDLKAWYCVSEGF DALRITKELLQEIGKFDSKDVHNNLNQLQVKLKE SLKGKKFLIVLD	282
HF L+ W CVS+ FD RIT+E+ +	D+ NLN LQV LKE ++G FL+VLD	
Sbjct: 214	HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLVLD	272
Query: 283	DVWNENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLF	341
DVWNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +		
Sbjct: 273	DVWNEDPVKWESSLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYVLEELTEDDSWSLIE	332
Query: 342	RHAFENMDPMG-HPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWRKILRSEIWE	400
H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE		
Sbjct: 333	SHSFREASCSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSIONLIQSTESK	392
Query: 401	LPH-NDILPALMLSYNDLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLVP-VKDE	457
+P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +		
Sbjct: 393	MPPAASDVL SALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESK	452
Query: 458	INQD LGNQYFLELRSRSLFEKVPNPSKRNIEELFLMHD LVNDLAQ LASSKLCIRLEESQ	517
++D+ + F +L R F R ++M+D V+DLA+ S R +E		
Sbjct: 453	RSEDMAEECFDDLVCRFFF-----RYSWGNYVMNDSVHDLARWVSLDEYFRADEDSP	504
Query: 518	SHMLEQCRHLSYSIGFNGEFKKLTPLYK-----LEQLRTLLPI-RIEFLHNLS	565
H+ + RHLS+ +++T + + L LRTLL + + EFR ++L		

Sbjct: 505 LHISKPIRHLWSWS-----ERITNVLEDNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLL 558
 Query: 566 KRVLHNILPTLRLSRLALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
 R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L
 Sbjct: 559 DRMFR----MLSIRVLDNSNCVIRNLPSSV-GNLKHLRYLGLSNTRIQRLPESVTRLCL 613
 Query: 626 LETLLLSSCADLEELPLQMEKLINLRHLDVSNTTLLKMPHLHSRLKSLQVLVGPFFVD- 684
 L+TLLL C +L LP M +L+ LR L +N + + RL LQ L + VD
 Sbjct: 614 LQTLLEGC-ELCRLPRSMSRLVQLRQLK-ANPDVIADIAKVGRILIELQELKA--YNVDK 669
 Query: 685 --GWRMEDLGEAQNLHGSLSVVKLENVVDRREAVKAKMREKNHVEQLSLEWSESSIADNS 742
 G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A
 Sbjct: 670 KKKGHGIAELSAMNQLHGDSLIRNLQNVEKTRESRKARLDEKQKLKLLDLRWADGRGAGEC 729
 Query: 743 QTESDILDELCPHKNIKKVEISGYRGTFNFPNWADPLFLKLVNLNLSRNCKDCYSLPALGQ 802
 + +L L PH N+++ I Y GT+ P+W+ D + + LR+C LP LGQ
 Sbjct: 730 DRDRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSARLTELPCLGQ 789
 Query: 803 LPCLKFLSVKGGMHIGIRVVTTEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWH--ALGIGEFP 860
 L L+ L + GM +R + +FYG F LE L M + +W FP
 Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSELLEWSEPRRNCCYFP 848
 Query: 861 TLENLSIKNCPELSLEIPIQFSSLKRLEVSDCPVFDDAQLFRSQLEAMKQIEEIDICDC 920
 L L I++CP L +P +L+ L +S +V + + + + +C
 Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTLEELRISRTGLVDPFGHNGDVTNVSLSSLHVSEC 907
 Query: 921 NSVTSFPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDCGCVDDISPEFLPTA- 979
 + S +L L ++ + DC ++ + E TA
 Sbjct: 908 RELRSLSEGLLQHNLVALKTA-----AFTDCDSLEFLPAEGFRTAI 948
 Query: 980 --RQLSIENCQNVTRFIPTATETLRISNC---ENVEKLSVACGGAAQMTSLNIWGXXX 1033
 L + NC FL+P++ E L++ C N + LS ++ L+I
 Sbjct: 949 SLESLIMTNCPLPCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDI---- 1003
 Query: 1034 XXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
 DCP + P L L + LVN QRL +
 Sbjct: 1004 -----KDCPNLSSFPPLCQLSALQHLSLVN-----CQRLQSI---- 1037
 Query: 1094 DGSDEDIEHWELPCSIQRLTIKNLKTLSSQHL-----KSLTSLQYLCI-----EG 1138
 ++ S++ LTI+N L+ H S T L + +G
 Sbjct: 1038 -----GFQALTSLESLTIQNCPLRTMSHSLVEVNNSDTGLAFNITRWMRRRTGDDG 1089
 Query: 1139 YL---XXXXXXXXXXXXHLSLQTLQIWN----FLNXXXXXXXXXXXXIDDPC 1190
 + HLT LQ L+I I DCP
 Sbjct: 1090 LMLRHRAQNDSSFFGGLLQHLTFLQFLKICQCPQLVFTGEEEKWRNLTSLQILHIVDCP 1149
 Query: 1191 NLQLSFESALPS--SLSQLFIQDCPNLQSLPFKGMPSSLSKLSIFNCPLLTPLEFDKGE 1248
 NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+
 Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFFPPGGVMSLAHLVIHECPQLCQRCDPGGD 1208
 Query: 1249 YWPQIAHAPII 1259
 WP IA++P I
 Sbjct: 1209 DWPLIANVPRI 1219

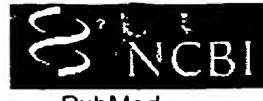
CPU time: 0.09 user secs. 0.01 sys. secs. 0.10 total secs.

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 10,906

Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 | expect: 10.000 | wordsize: 3 | Filter |

DovArt

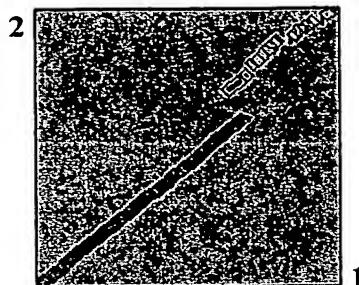
Clawed

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

DB

Seq101b2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

Query: 1 MEIGLAVGGAFLSSALNVLFDR LAPNGD LLMFRXXXXXXXXXXMTL RG IQIVL SDA 60

M L +GG F S + L D+ A N + + R LR I +L A

Sbjct: 1 MSTALVIGGWFAQSFI QTLLDK-ASNCAIQQLARRGLHDDLRLRTSLLR-IHAILDKA 58

Query: 61 ENK-QASNPSVRDWLNELRDAVDSAENLIEEVNYEALRLKVEGQHQNFSETSNNQVS--- 116

E + N S+ + + L+DA AE+L+EE+ Y+A + KVE + S+ + + S

Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTAS 118

Query: 117 -----DDFFLNIKDKLEDTIETLKD LQE QIG L LGLKE---YFDSTKLETRRPSTS VDD 166

DD + + + D+ + + L L + FD + RR + + S

Sbjct: 119 EWLGADGDDAGTRLREI QGKLCNIAADMMDVMQL LAPDDGGRQFDWKVV--RRETSSFLT 176

Query: 167 ESDIFGRQSEIEDLIDRLLSEGASGKKLTVVPIVGMGGQGKTTLAKAVYNDERVKNHFDL 226

E+ +FGR E E + + + LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L

Sbjct: 177 ETVVFG RDQEREKV VELL L DSGSGN SFSV L P L V GIGGVGKTTLA QLVYNDNRVG NYFHL 236

Query: 227 KAWYC VSEGFDALRITKELLQ EIGKFD SKDVHNNLNQLQVKL KESLKGKKFLIVLDDVWN 286

K W CVS+ F+ R+TKE++ + K + D NL+ LQ LKE + + + FL+VLDDVW+

Sbjct: 237 KVWVCVSDNFNVKRLTKEIIESATKVEQSD-KLNLDLTLQ QILKEKIASERFLLVLDDVWS 295

Query: 287 ENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQRHAF 345

EN + + W L GSK+IVTTR + A + + G + + I + L + A W LF++ AF

Sbjct: 296 ENRDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAF 355

Query: 346 ENMDPMGHPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWKRILRSEI WELP--H 403

+++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP

Sbjct: 356 GSVNPQEHLELEVIGRKIA GKLKGSP LA AKTLGSLLRDVSQEHWRTIMESEVWQLPQAE 415

Query: 404 NDILPALMLS YNDLPAHLKRCFS FCAIFPKD YPFRKEQVIHLWIANGLVPVK-DEINQDL 462

N+ILP L LSY LP HL+ +CF+FCA+F KDY F K + + I WIA G + + + + + D+

Sbjct: 416 NEILPVLWLSYQHLPGHLRQCFACAVFHKDYL FYKHELIQTWIAEGFIAHQGNKRMEDV 475

Query: 463 GNQYFLELRSRSRSLF EKV PNPSKR NIEELFLMHD LVNDLAQ LASSKLCIRLEESQGSHMLE 522

G+ YF EL +RS F+ + + + MHDL++ DLAQ S C R+++ +

Subjct: 476 GSSYFHELVNRSFFQ-----ESRWRGRYVMHDLIHDLAQFISVGECRIDDKSKEPS 529

Query: 523 QCRHLSYSIGFNGEFKKLTPLYKLEQLRTLLPIRIEFLRHLNLSK---RVLHNILPTLRS 578
RHLS ++ E KL +LRTL+ + ++K + H++ L+

Subjct: 530 TTRHLSVAL---TEQMKLVDFSGYNKLRTLMINNQRNQYPYMTKVNSCLLPHSLFKRLKR 586

Query: 579 LRALSFSQYKIKELPNLFTKLKLLRFLDIS-RTWITKLPDSICGLYNLETLLLSSCADL 637
+ L + +KELP D+ L LR+LDIS I +LP+S+C LYNL+ L L C L

Subjct: 587 IHVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQLPESLCDLYNLQALRLWGC-QL 644

Query: 638 EELPLQMEKLIINLRHLDVSNTRRLKMPHLHSRLKSLQVLVGPFFVD-GWRMEDLGEAQN 696
P M KLINLR L V + K+ + +L SLQ L K + G ++ +L

Subjct: 645 RSFPQGMSKLIINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVLNNHGNKLAELSGLTQ 703

Query: 697 LHGSLSVVKLENVVDRREAVKAKMREKNHVEQLSLEWSE---SSIADNSQTESDILDELC 753
L +L + LENV + EA KAK+ K ++E L LEW+ SS+ ++L L

Subjct: 704 LRSTLRITNLENVGSKKEASKAKLHRKQYLEALELEWAAGQVSSLEHELLVSEEVLLGLQ 763

Query: 754 PHKNIKKVEISGYRGTNFPNVADPLFLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKG 813
PH +K + I GY G P+W+ + L L L NC L +GQLP LK L +K

Subjct: 764 PHHFLKSLSLTIRGYSATVPSWLDVKMLPNLGLTLENCTRLEGLSYIGQLPHLKVLHMKR 823

Query: 814 MHGIRVVTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWHALGIGEFPTLENLSIKN 869
M ++ ++ E G SK F LE+L EDM K++ + + P L+ + +KN

Subjct: 824 MPVVKQMSHELCGCTKSCL-FPRLEELVLEDMPYLKEFP--NLAQLPCLKIIHMKN 876

Score = 79.3 bits (194), Expect = 1e-12

Identities = 124/517 (23%), Positives = 191/517 (35%), Gaps = 142/517 (27%)



Query: 780 FLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKGHMHIRVVTEEFYGRLLSSKKPFNSLEK 839
F +L L ++ L +L +LPCLK +KG+ ++ + + + + F LE

Subjct: 997 FPRLEELIKGMLTFEELHSLEKLPCLKVFRIKGLPAVKKIGHGLFDSTCQRECFFPRLED 1056

Query: 840 LEFEDMTEWKQWHALGIGE-FPTLENLSIKNCPELSLEIPIQFS----- 882
L DM W++W E F L L I+ CP+L +PI S

Subjct: 1057 LVLSDMPAWEWSWAEREELFSCLCRLKIEQCPKLKCLLPIPHSLIKLELWQVGLTGLPG 1116

Query: 883 -----SLKRLEVSDCPVVFDDAQLFRSQLEAMKQIEEIDICDCNSVTSFPF 928
SL L + CP ++ + S + I I I +C + P

Subjct: 1117 LCKGIGGGSSTRASLSSLHIKCPNLRNLGEGLLS--NHLPHINAIRIWECAELLWLPV 1174

Query: 929 SILP--TTLKRIQISRCPKLKLEAPVGE-----MFVEYLRVNDCGCVDDISP---EFLP 977
TTL+ + I CPKL E ++ L + DCG + P L

Subjct: 1175 KRFREFTTLENLSIRNCPKLMSMTQCEENDLLLPLLIKALELGDCGNLGKSLPGCLHNLS 1234

Query: 978 TARQLSIENCQ--NVTRFLIPTATE--TLRISNCENVEKLSVACGAAQMITSNIWGXX 1032
+ QL+I NC ++ R ++ E T+RI NC+ +

Subjct: 1235 SLTQLAISNCPYMVSLSLPREVMLHLKELGTVRIENCGL----- 1272

Query: 1033 XXXXXXXXXXXXXXXXXDCPEIEG-ELPFNLEILRIIYCKKLV--NGRKEWHLQRLTEL 1089
IEG ++ +L+ L II C +L+ G ++ + L EL

Subjct: 1273 -----GSIEGLQVLKSLKRLAIIGCPRLLNNEGDEQGEVLSLLEL 1312

Query: 1090 WIDHDGSDDEDIEHWELPCSIQRLTIKNLKTLSSQH-LKSLTSLQYLCIEGYLXXXXXX 1148
+D ++ IKN TL H L+ + S Q + +

Subjct: 1313 SVDK-----TALLKLSLIKNTLPFIHSLRIIWSPQKVMFD-----LEE 1350

Query: 1149 XXXXXHLTSLQTLQIWNFLNXXXXXXXXXXXXIDDCPNLQSL-FESALPSSLSQL 1207
LT+L+ L+ + C NLQSL E SL L

Subjct: 1351 QELVHSLTALRRLEFFR-----CKNLQSLPTELHTLPSLHAL 1387

Query: 1208 FIQDCPNLQSLPFPKGMPSSLSKLSIFNC-PLLTPLL 1243
+ DCP +QSLP KG+P+ L+ L +C P+LT LE

Subjct: 1388 VVSDCPQIQSLPEKGLPTLLTDGFHDCHPVLTAQLE 1424

CPU time: 0.20 user secs. 0.01 sys. secs. 0.21 total secs.

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 13,460
Number of extensions: 8847
Number of successful extensions: 46
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)





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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 | expect: 10.000 | wordsize: 3 | Filter |

Prior Art

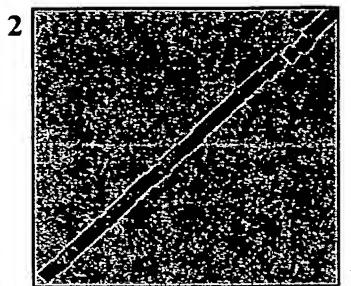
Claimed

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D3

Seq ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49 TLRGIQIVLSDAENKQASNPSVRDWLNELRAVDSAENLIEEVNYEALRLKVEGQHQNF 108

TL +L +A+ ++ +S+ WL EL++ A+++++E A+RLKV +

Sbjct: 46 TLLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKV-----T 98

Query: 109 ETSNQQVSDDFFLNIK--DKLEDTIETLKDL---QEIQIGLLGLKEYFDSTKLETRRPST 162

++ +++ D +N+ K+ D + L + + G L + DSTK R +T

Sbjct: 99 RSTFKRLIDHVIINVPLAHKVADIRKRLNGVTLERELNLGALEGSQPLDSTK---RGVTT 155

Query: 163 SVDDESDIFGRQSEIEDLIDRLLSEGASGKLLTVVPIVGMGGQGKTTLAKAVYNDERVKN 222

S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+

Sbjct: 156 SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVPIVGLGGAGKTTSQLIFNDKRVEE 213

Query: 223 HFDLKAWYCVSEGFDALRITKELLQEIGKFDSKDVHNNLNQLQVKLKESSLKGKKFLIVLD 282

HF L+ W CVS+ FD RIT+E+ + D+ NLN LQV LKE ++G FL+VLD

Sbjct: 214 HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLVLD 272

Query: 283 DVWNENYNEWNDLRNIFAQGDIGSKIIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQ 341

DVWNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +

Sbjct: 273 DVWNEDPVKWESELLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYVLEELTEDDSWSLIE 332

Query: 342 RHAFENMDPMG-HPELEEVGRQIAAKCKGLPLALKTLAGMLRSKSEVEEWKRILRSEIWE 400

H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE

Sbjct: 333 SHSFREASCSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSIONLQSTESK 392

Query: 401 LPH--NDILPALMLSYNDLPAHLKRCFSFCAIFPKDYPFRRKEQVIHLWIANGLVP-VKDE 457

+P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +

Sbjct: 393 MPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESK 452

Query: 458 INQD LGNQYFLELRSRSLFEKVPNPSKRNIEELFLMHDVLNDAQLASSKLCIRLEESQG 517

++D+ + F +L R F R ++M+D V+DLA+ S R +E

Sbjct: 453 RSEDMAEECFDDLVCRFFF-----RYSWGNYVMNDSVHDLARWVSLDEYFRADEDSP 504

Query: 518 SHMLEQCRHLSYSIGFNGEFKKLTPLYK-----LEQLRTLLPI-RIEFLHNL 565

H+ + RHLS+ +++T + + L LRTLL + + EFR ++L

Blast Result

Sl jct: 505 LHSKPIRHLSWCS-----ERITNVLEDNNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLL 558

Query: 566 KRVLNILPTLRLSRLALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L

Sbjct: 559 DRMFR---MLSIRVLDFSNCVIRNLPPSSV-GNLKHLRYLGLSNTRIQRLPESVTRLCL 613

Query: 626 LETLLLSSCADLEELPLQMEKLINLRHLDVSNTRRLKMLHLSRLKSLQVLVGPFFVD- 684
L+TLLL C +L LP M +L+ LR L +N + + RL LQ L + VD

Sbjct: 614 LQTLLLEGCA-ELCRLPRSMSRLVKLRLQLK-ANPDVIADIAKVGRILIELQELKA--YNVDK 669

Query: 685 --GWRMEDLGAEQNLHGSLSVVKLENVVDRREAVKAKMREKNHVEQLSLEWSSESSIADNS 742
G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A

Sbjct: 670 KKGHGIAELSAMNQLHGDSLIRNLQNVEKTRSRKARLDEKQKLKLLDLRWADGRGAGEC 729

Query: 743 QTESDILDELCPHKNIKKVEISGYRGTFNPNWVADPLFLKLVNLSLRNCKDCYSLPALGQ 802
+ +L L PH N++++ I Y GT+ P+W+ D + + LR+C LP LGQ

Sbjct: 730 DRDRKVLKGLRPHPNLRELSIKYGGTSSPSWMTDQYLPNMETIRLRCARLTELPCLGQ 789

Query: 803 LPCLKFLSVKGHMIGIRVVTTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWH--ALGIGEFP 860
L L+ L + GM +R + +FYGF LE L M + +W FP

Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSELWSEPRRNCCYFP 848

Query: 861 TLENLSIKNCPELSLEIPIQFSSLKRLEVSDCPVVFDDAQLFRSQLEAMKQIEEIDICDC 920
L L I++CP L +P +L+ L +S +V + + + + +C

Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTEELRISRTGLVDPFGHNGDVTTNVSLSSLHVSEC 907

Query: 921 NSVTSPPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDCGCVDDISPEFLPTA- 979
+ S +L L ++ + DC ++ + E TA

Sbjct: 908 RELRSLSEGLLQHNLVALKTA-----AFTDCDSLEFLPAEGFRTAI 948

Query: 980 --RQLSIENCQNVTRFIPTATETLRISNC---ENVEKLSVACGGAAQMTSNLIWXXX 1033
L + NC FL+P++ E L++ C N + LS ++ L+I

Sbjct: 949 SLESLIMITNCPLPCSFLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDI---- 1003

Query: 1034 XXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
DCP + P L L + LVN QRL +

Sbjct: 1004 -----KDCPNLSSFPFPGLCQLSALQHLSLVN-----CQRLQSI---- 1037

Query: 1094 DGSDEDIEHWELPCSIQRLTIKNLKTLSSQHL----KSLTSLQYLCI-----EG 1138
++ S++ LTI+N L+ H S T L + +G

Sbjct: 1038 -----GFQALTSLESLTIQNCPRLTMSHLVEVNNSSDTGLAFNITRWMRRRTGDDG 1089

Query: 1139 YL---XXXXXXXXXXXXHLSLQTLQIWN----FLNXXXXXXXXXXXXIDDCP 1190
+ HLT LQ L+I I DCP

Sbjct: 1090 LMLRHRAQNDSSFGGLLQHLTFLQFLKICQCPQLVTFTGEEEKWRNLTSLQILHIVDCP 1149

Query: 1191 NLQSLFESALPS--SLSQLFIQDCPNLQSLPFKGMPSSLSKLSIFNCPLLTPLEFDKGE 1248
NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+

Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFFPGGVMSLAHLVIHECPQLCQRCDPGGD 1208

Query: 1249 YWPQIAHIPII 1259
WP IA++P I

Sbjct: 1209 DWPLIANVPRI 1219

CPU time: 0.08 user secs. 0.02 sys. secs 0.10 total secs.

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 10,906

Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
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Matrix BLOSUM62 gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

Prior Art

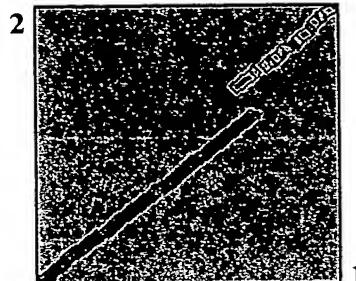
Claimed

Sequence 1 lcl|seq_1 Length 1220 (1 .. 1220)

D4

Seq 18N0:2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 401 bits (1031), Expect = e-109
 Identities = 300/911 (32%), Positives = 463/911 (49%), Gaps = 69/911 (7%)

Query: 1 MEIGLAIGGAFLSSALNVLFDR LAPNGD LLMFRKHTDDV E L F E K L G D I L L S L Q I V L S D A 60
 M L I G G F S + L D + A N + + R + + L + L L + + L A
 Sbjct: 1 M S T A L V I G G W F A Q S F I Q T L L D K - A S N C A I Q Q L A R R R G L H D D L - R R L R T S L L R I H A I L D K A 58

Query: 61 E N K - K A S N Q F V S Q W L H K L Q T A V D A A E N L I E Q V N Y E A L R L K V E T S N Q V S D L - - - N L C L S D 116
 E + N + + + + L + A A E + L + E + + Y + A + K V E Q + S D L + L +
 Sbjct: 59 E T R W N H K N T S L V E L V R Q L K D A A Y D A E D L L E E L E Y Q A A K Q K V E H R G D Q I S D L F S F S L S T A S 118

Query: 117 D F F - - - - - L N I K K K L - - - E D T I K K L E V L E K Q I G R G L K E H F I S T K Q E T R T P S T 161
 + + I + K L D + + + + L G G G + + + + E T +
 Sbjct: 119 E W L G A D G D D A G T R L R E I Q G K L C N I A A D M M D V M Q L L A P D D G - - G R Q F D W K V V R R E T - - - S 172

Query: 162 S L V D D S G I F G R K N E I E N L V G R L L S M D T K R K N L A V V P I V G M G G M G K T T L A K A V Y N D E R V Q K 221
 S + + + + F G R E E + V L L + + + V + P + V G + G G + G K T T L A + V Y N D R V
 Sbjct: 173 S F L T E T V V F G R D Q E R E K V V E L L L D S G S G N S S F S V L P L V G I G G V G K T T L A Q L V Y N D N R V G N 232

Query: 222 H F G L T A W F C V S E A Y D A F R I T K G L L Q E I G S T D L K A D D N L N Q L Q V K L K A D D N L N Q L Q V K L K E 281
 + F L W C V S + + + R + T K + + + T + + D L N . L + L Q L K E
 Sbjct: 233 Y F H L K V W V C V S D N F N V K R L T K E I I E S - - A T K V E Q S D K L N - - - - - L D T L Q Q I L K E 279

Query: 282 K L N G K R F L V V L D D V W N D N Y P E W D D L R N L F L Q G D I G S K I I V T T R K E S V A L M M D S - G A I Y M G 340
 K + + R F L + V L D D V W + + N + W + L G S K + I V T T R + A + + + I +
 Sbjct: 280 K I A S E R F L L V L D D V W S E N R D D W E R L C A P L R F A A R G S K V I V T T R D T K I A S I I G T M K E I S L D 339

Query: 341 I L S S E D S W A L F K R H S L E H K D P K E H P E F E E V G K Q I A D X X X X X X X X X X R S K S E V D E 400
 L + W L F K + + + P + E H E E + G + + I A R +
 Sbjct: 340 G L Q D D A Y W E L F K K C A F G S V N P Q E H L E L E V I G R K I A G K L K G S P L A A K T L G S L L R L D V S Q E H 399

Query: 401 W R N I L R S E I W E L P C S N G I L P A L M S Y N D L P A H L K Q C F A Y C A I Y P K D Y Q F R K E Q V I H L W I 460
 W R I + S E + W + L P N I L P L L S Y L P H L + Q C F A + C A + + K D Y F K + + I W I
 Sbjct: 400 W R T I M E S E V W Q L P Q A E N E I L P V L W L S Y Q H L P G H L R Q C F A V F H K D Y L F Y K H E L I Q T W I 459

Query: 461 A N G L V - H Q F H S - - - G N Q Y F I E L R S R S L F E M A S E P S E R D V E E F L M H D L V N D L A Q I A S S N 514
 A G + H Q + G + Y F E L + R S F + R + + M H D L + + D L A Q S

Sbjct: 460 AEGFIAHQGNKRMEDVGSSYFHELVNRSFFQ----ESWRGRYVMHDLIHDLAQFISVG 514

Query: 515 HCIRLEDNKGSMLEQCRHMSYSIGQDGEFEKLKSLFKSEQLRTLLPID--IQFHYSKKL 572
C R++D+K RH+S ++ E KL +LRTL+ + Q+ Y K+

Sbjct: 515 ECHRIIDDKSKETPSTTRHLSVAL---TEQMKLVDGSGYNKLRTLMINNQRNQYPYMTKV 571

Query: 573 SKRVL-HNILPTLRLSRLALSLSHYQIEVLPNDLFIKLKLLRFLDLS-ETSITKLPSIFV 630
+ +L H++ L+ + L L ++ LP D+ L LR+LD+S I +LP+S+

Sbjct: 572 NSCLLPHSLFKRLKRIHVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQRLPESLCD 630

Query: 631 LYNXXXXXXXXXXXXXXXXXXXXQMEKLINLRHLDISNTRRLKMPHLHSRLKSLQVLVGAKFL 690
LYN M KLINLR L + + K+ + +L SLQ L K L

Sbjct: 631 LYNLQALRLWGCQLRSFPQG-MSKLINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVL 688

Query: 691 VG-GWRMEYLGEAHNLYGSLSILELENVDRREAVKAKMREKNHVEQLSLEWSE--SIS 746
G ++ L L +L I LENV + EA KAK+ K ++E L LEW+ S

Sbjct: 689 NNHGNKLAELSGLTQLRSTLRITNLENVGSKEEASKAKLHRKQYLEALELEWAAGQVSSL 748

Query: 747 ADNSQTERDILDELPHKNIKAVEITGYRGTNFPNWADPLFVVLVHLYLRNCKDCYSLP 806
++L L+PH +K++ I GY G P+W+ + L L L NC L

Sbjct: 749 EHLLVSEEVLLGLQPHHFLKSLTIRGYSATVPSWLDVKMLPNLGLTLKLENCTRLEGLS 808

Query: 807 ALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVKLRFEDMPEWKQWHTLGIGE 866
+GQLP L+ L ++ M ++ ++ E G SK F L +L EDMP K++ L +

Sbjct: 809 YIGQLPHLKVLHMKRMPVVKQMSHELCGCTKSKL-FPRLEELVLEDMPNLKEFPNL--AQ 865

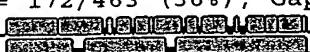
Query: 867 FPTLEKLSIKN 877

P L+ + +KN

Sbjct: 866 LPCLKIIHMKN 876

Score = 71.6 bits (174), Expect = 2e-10

Identities = 110/463 (23%), Positives = 172/463 (36%), Gaps = 88/463 (19%)



Query: 788 FVKLVHLYLRNCKDCYSLPALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVK 847
F +L L ++ L +L +LPCL+ I+G+ ++ + + + + F L

Sbjct: 997 FPRLEELIKGMLTFEELHSLEKLPCLKVFRIKGLPAVKKIGHGLFDSTCQRECFPRLED 1056

Query: 848 LRFEDMPEWKQWHTLGIGE-FPTLEKLSIKNCPELSLEIPIQFSSLKRLDICDCKSVTSF 906
L DMP W++W E F L +L I+ CP+L +PI

Sbjct: 1057 LVLSDMPAWEEWSWAEREELFSCLCRLKIEQCPKLKCLLPI----- 1097

Query: 907 PFSILPTTLKRIKISGCPKLKLEAPVGE---MFVEYLSVIDC---GCVDDISPEFLPT 958
P S++ L ++ ++G P L G + L +I C + + + LP

Sbjct: 1098 PHSLIKLELWQVGLTGLPGLCKGIGGGSSRTASLSLLHIICKPNLRNLGEGLLSNHLPH 1157

Query: 959 ARQLSIENCHN----VTRFLIPTATESLHIRNCEKL-SMA-CGGAAQLTSNLIWGXXXX 1011
+ I C V RF T E+L IRNC KL SM C L I

Sbjct: 1158 INAIRIWECAELLWLPVKRFREFTTLENLSIRNCPKLMSMTQCEENDLLLPLLIKALELG 1217

Query: 1012 XXXXXXXXXXXXXXXTYCPEIEGELP----FNLQILDIFYCKKLVNGRKE--WHLQRL 1063
C + LP +L L I C +V+ +E HL+ L

Sbjct: 1218 D-----CGNLGKSLPGCLHNLSSLTQLAISNCPYMVSLSPREVMLHLKEL 1261

Query: 1064 TELWIKHGSDEHIEHWELPSSIQRLFIFNL-----KTLSSQHL----- 1102
+ I++ IE ++ S++RL I + LS L

Sbjct: 1262 GTVRIENCDGLGSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKTALLK 1321

Query: 1103 ----KSLTSQFLRIVGNXXXXXXXXXX-LTSLQTLQIWNFLNXXXX-XXXXXX 1155
+L + LRI+ + H LT+L+ L+ + N

Sbjct: 1322 LSLIKNTLPFIHSLRIIWSQPKVMDLEEQELVHSLTALRRLEFFRCKNLQSLPTELHTL 1381

Query: 1156 XXXXXIIISNCPNLQSLPLKGMPSSLSTLSISKC-PLLTPLLE 1197
++S+CP +QSLP KG+P+ L+ L C P+LT LE

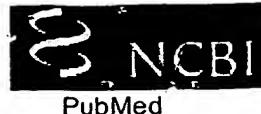
Sbjct: 1382 PSLHALVVSDCPQIQSLPEKGLPTLTDLGFHDHCHPVLTAQLE 1424

CPU time: 0.16 user secs. 0.00 sys. secs. 0.16 total secs.

Lambda K H
0.320 0.137 0.406

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 12,261
Number of extensions: 8166
Number of successful extensions: 28
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1220
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1078
Effective length of database: 765,046,036
Effective search space: 824719626808
Effective search space used: 824719626808
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

Prior Art

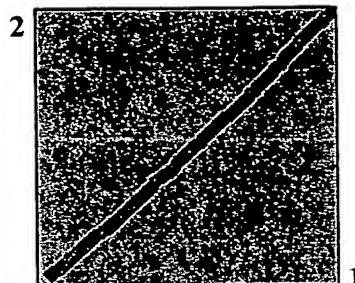
Claimed

Seq ID: 4

Sequence 1 lcl|seq_1 Length 1220 (1 .. 1220)

D4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 399 bits (1024), Expect = e-109
 Identities = 352/1233 (28%), Positives = 552/1233 (44%), Gaps = 129/1233 (10%)

Query: 50	LLSLQIVLSDAENKKASNQFVSQWLHKLQTAVDAEENLIEQVNYEALRLKVETSNQQVSD	109
Sbjct: 47	LLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAIRLKVRSTFKR--	104
Query: 110	LNLCLSDDFFLNIK--KKLEDTIKKLE--VLEKQIGRLGLKEHFISTKQETRTPSTSLVD	165
Sbjct: 105	L D +N+ K+ D K+L LE++ LG E R +TSL+	159
Query: 166	DSGIFGRKNEIENLVGRLLSMDTKRKNLAVVPIVGMMGGKTTLAKAVYNDERVQKHGGL	225
Sbjct: 160	+S I GR + ENL+ LL + VVPIVG+GG GKTTL++ ++ND+RV++HF L ESCIVGRAQDKENLIRLLL--EPSDGAVPVVPIVGLGGAGKTTLSQLIFNDKRVEEHFPL	217
Query: 226	TAWFCVSEAYDAFRITKGLLQEIGSTDLKADDNLNQLQVQLKADDNLNQLQVQLKEKLNG	285
Sbjct: 218	W CVS+ +D RIT+ + T+ + L NLN LQV LKE++ G RMWVCVSDDFDVKRITREI-----TEYATNGRFMDLT-----NLNMLQVNKEEIRG	264
Query: 286	KRFLVVLDDVVNDNYPEWDDLRNLFLQGDIGSKIIVTTRKESVALMMDSGAIY-MGILSS	344
Sbjct: 265	FL+VLDDVVNN++ +W+ L G GS +IVTT+ + VA + + Y + L+ TTFLLVLDVVWNEDPVWKWESLLAPLDAGGRGSVVIVTTQSKVADVTGTMEPYVLEELTE	324
Query: 345	EDSWALFKRHS-EHKDPKEHPEFEEVGKQIADXXXXXXXXXXXXXRSKSEVDEWRN	403
Sbjct: 325	+DSW+L + HS E +P EE+G++IA RSK WR DDSWSLIESHSFREASCSSSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWRE	384
Query: 404	ILRSEIWELPSCSNGILPALMLSNDLPAHLKQCFAYCAIYPKDYQFRKEQVIHLWIANG	463
Sbjct: 385	+L +E WE+P ++ +L AL SY++LP LK CFA+CA++ K Y+FRK+ +IH+WIA VLETETWEMPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYFRKDTLIHMWIAQN	444
Query: 464	LVHQFHS-----GNQYFIELRSRSLFEMASEP SERDVEEFLMHDLVNDLAQIASSNHC	517
Sbjct: 445	L+ S + F +L R F + ++M+D V+DLA+ S + LIQSTESKRSEDMAEECFDDLVCRFFFYRSG-----NYVMNDSVHDLARWVSLDEYF	497
Query: 518	RLEDNKGSHMLEQCRHMSYSIGQDGEFEKLKSLFKSEQ-----LRTLLPIDIQF	566
	R +++ H+ + RH+S+ E++ ++ + LRTLL +	

Sbjct: 498 RADEDSPHLISKPIRHLWSWC-----ERITNVLEDNNNTGGDAVNPLSSLRTLLFLG--- 548
 Query: 567 HYSKKLSKRVLHNILPTLRLSRLRALSLSHYQIEVLPNDLFIKLKLLRFLDLSETSITKLPD 626
 S+ S +L + L +R L S+ I LP+ + LK LR+L LS T I +LP+
 Sbjct: 549 -QSEFRSYHLLDRMFRMLSIRVLDFSNCVIRNLPSVG-NLKHLRYLGLSNTRIQLP 606
 S+ L M +L+ LR L DI+ RL + L L
 Sbjct: 607 SVTRLC-LLQTLLLEGCELCLRPRSMRSLVKLRLKANPDVIADIAKVGR 662
 S+ L M +L+ LR L DI+ RL + L L
 Query: 627 SIFVLYNXXXXXXXXXXXXXXQMEKLINLRHL-----DISNTRRLKMPHLHSRL 678
 S+ L M +L+ LR L DI+ RL + L L
 Sbjct: 607 SVTRLC-LLQTLLLEGCELCLRPRSMRSLVKLRLKANPDVIADIAKVGR 662
 S+ L M +L+ LR L DI+ RL + L L
 Query: 679 KSLQVLVGAKFLVGGWRMEYLGEAHNLGSLISILELENVDRREAVKAKMREKNHVEQLS 738
 K+ V G + L + L+G LSI L+NV RE+ KA++ EK ++ L
 Sbjct: 663 KAYNVDKKK----GHGIAELSAMNQLHGDLSIRNLQNEKTRSRKARLDEKQKLKLD 717
 S+ L M +L+ LR L DI+ RL + L L
 Query: 739 LEWSE SISADNSQTERDILDEL RPHKNIKAVEITGYRGTNFPNWADPLFVKLVHLYLRN 798
 L W++ A +R +L LRPH N++ + I Y GT+ P+W+ D + + LR+
 Sbjct: 718 LRWADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRS 777
 S+ L M +L+ LR L DI+ RL + L L
 Query: 799 CKDCYSLPALGQLPCLEFLSIRGMHGIRVVTTEFYGRLLSSKKPFNSLVKLRFEDMPEWKQ 858
 C LP LGQL L L I GM +R + +FYG F L L MP ++
 Sbjct: 778 CARLTELPCLGQLHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSEE 836
 S+ L M +L+ LR L DI+ RL + L L
 Query: 859 WH--TLGIGEFPTLEKLSIKNCPEL---SLEIPIQFSSLKRLDICDCKSVTSFPPFSILP 912
 W FP L KL I++CP L SL ++ + R + D
 Sbjct: 837 WSEPRRNCCYFPRLHKLIEDCPRLRNLPSPPTLEELRISRTGLVLDLPGFHGNGDVTN 896
 S+ L M +L+ LR L DI+ RL + L L
 Query: 913 TTLKRIKISGCPKLKLEAPVGEMFVEYLSVIDCGCVDDISPEFLP-----TARQLSI 964
 +L + +S C +L+ G + +++ D S EFLP + L +
 Sbjct: 897 VSLSSLHVSECRELR-SLSEGLLQHNLVALKTAFTDCDSLEFLPAEGFRTAISLESIM 955
 S+ L M +L+ LR L DI+ RL + L L
 Query: 965 ENCHNVTRFLIPTATESLHIRNC-----EKLSMACGGAAQLTLSNIWGXXXXXX--- 1014
 NC FL+P++ E L ++ C + LS L+ L+I
 Sbjct: 956 TNCPLPCSFLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDIKDCPNLSSFPPG 1015
 S+ L M +L+ LR L DI+ RL + L L
 Query: 1015 -XXXXXXXXXXTYCPEIEG---ELPFNLQILDIRYCKKL-----VNGRKEWHLQR 1062
 C ++ + +L+ L I+ C +L VN + L
 Sbjct: 1016 PLCQLSALQHLSLVNCQRLQSIGFQALTSLESLTIQNCPRLTMSHSLVEVNNSSDTGLAF 1075
 S+ L M +L+ LR L DI+ RL + L L
 Query: 1063 LTELWIKHGSDEHIEHWELPSSIQRLFIFNLKTLSSQHLKSLTSQFLRIVG-NXXXXX 1121
 W++ D+ + L Q F L+ LT LQFL+I
 Sbjct: 1076 NITRWMRRRTGDDGL---MLRHRAQNDSFF-----GGLLQHLTFLQFLKICQCPQLVTF 1126
 S+ L M +L+ LR L DI+ RL + L L
 Query: 1122 XXXXXXXXXHLSLQTLQIWNFLNXXXXXXXXXXXXX- ISNCPNLQSLPLKGMPSS 1180
 +LTSLQ L I + N + I CP + + P G+ S
 Sbjct: 1127 TGEEEKWRNLTSQILHIVDCPNLEVLPANLQSLCSLSTLYIVRCPRIHAFPPGGVSMS 1186
 S+ L M +L+ LR L DI+ RL + L L
 Query: 1181 LSTLSISKCPPLTLPLEFDKGEYWTEIAHIPTI 1213
 L+ L I +CP L + G+ W IA++P I
 Sbjct: 1187 LAHLVIHECPQLCQRCDDPVGDDWPLIANVPRI 1219
 S+ L M +L+ LR L DI+ RL + L L

CPU time: 0.09 user secs. 0.01 sys. secs. 0.10 total secs.

Lambda K H
0.320 0.137 0.406

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 9918
 Number of extensions: 6581
 Number of successful extensions: 26
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1220
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1078
Effective length of database: 765,046,036
Effective search space: 824719626808
Effective search space used: 824719626808
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 | gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

Nov 2004

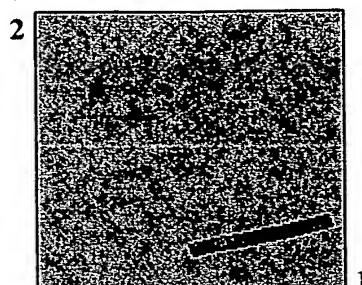
Claimed

Sequence 1 lcl|seq_1 Length 318 (1 .. 318)

D5

~~88~~ 100:2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 34.3 bits (77), Expect = 6.9

Identities = 31/149 (20%), Positives = 66/149 (43%), Gaps = 6/149 (4%)

Query: 159 SIIGVHGLGGVGXXXXXXXXXXXXXXRDYHVVIMIEVANSETLNVDMQK-IIANRLA 217
S++ + G+GGVG +H+ + + V S+ NV + K II +
Sbjct: 205 SVLPLVGIGGVGKTTLAQLVYNDNRVGNY-FHLKVWVCV-SDNFNVKRLTKEIIESATK 261

Query: 218 LPWNESETERERSTYLRRALRRKKFVVLDDVW-KKFQLADVGIPTPSSDKGCKLILAS 275
+ ++ L+ + ++F++LDDVW + + P + +G K+I+ +
Sbjct: 262 VEQSDKLNLDTLQQILKEKIASERFLLVLDVVSENRDDWERLCAPLRFAARGSKVIVTT 321

Query: 276 RSNQVCVEMGDKEPMEMPCLDNNESSLRLF 304

R ++ +G + + + L D+ LF

Sbjct: 322 RDTKIASIIGTMKEISLDGLQDDAYWELF 350

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H
0.319 0.135 0.400

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 2615

Number of extensions: 1870

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's gapped: 2

Number of HSP's successfully gapped: 1

Number of extra gapped extensions for HSPs above 10.0: 1

Length of query: 318

Length of database: 765,046,178
Length adjustment: 130
Effective length of query: 188
Effective length of database: 765,046,048
Effective search space: 143828657024
Effective search space used: 143828657024
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 76 (33.9 bits)



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 | gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter Align

Print

Claimed

Sequence 1 lcl|seq_1 Length 318

DS

Sequence 2 lcl|seq_2 Length 1232

SOA ID No: 4

No significant similarity was found

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